

1652

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/595,682A

DATE: 05/07/2001  
TIME: 17:38:03

Input Set : A:\Sj-0005.app  
Output Set: N:\CRF3\05072001\I595682A.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Danks, Mary K.  
4 Potter, Philip M.  
5 Houghton, Peter J.  
7 <120> TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting  
8 Growth of Human Tumor Cells  
10 <130> FILE REFERENCE: SJ-0005  
12 <140> CURRENT APPLICATION NUMBER: 09/595,682A  
13 <141> CURRENT FILING DATE: 2000-06-16  
15 <150> PRIOR APPLICATION NUMBER: 60/075,258  
16 <151> PRIOR FILING DATE: 1998-02-19  
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/03171  
19 <151> PRIOR FILING DATE: 1999-02-12  
21 <160> NUMBER OF SEQ ID NOS: 30  
23 <170> SOFTWARE: PatentIn Ver. 2.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 34  
27 <212> TYPE: PRT  
28 <213> ORGANISM: Artificial Sequence  
30 <220> FEATURE:  
31 <221> NAME/KEY: UNSURE  
32 <222> LOCATION: (7)  
34 <220> FEATURE:  
35 <221> NAME/KEY: UNSURE  
36 <222> LOCATION: (33)  
38 <220> FEATURE:  
39 <221> NAME/KEY: UNSURE  
40 <222> LOCATION: (22)  
W--> 42 <223> OTHER INFORMATION:  
42 <400> SEQUENCE: 1  
W--> 43 His Pro Ser Ala Pro Val Xaa Val Asp Thr Val His Gly Lys Val Leu  
44 1 5 10 15  
W--> 46 Gly Lys Phe Val Ser Xaa Glu Gly Phe Ala Gln Pro Val Ala Lys Phe  
47 20 25 30  
W--> 49 Xaa Gly  
53 <210> SEQ ID NO: 2  
54 <211> LENGTH: 36  
55 <212> TYPE: PRT  
56 <213> ORGANISM: Oryctolagus cuniculus  
58 <400> SEQUENCE: 2  
59 His Pro Ser Ala Pro Pro Val Val Asp Thr Val Lys Gly Lys Val Leu  
60 1 5 10 15  
62 Gly Lys Phe Val Ser Leu Glu Gly Phe Ala Gln Pro Val Ala Val Phe  
63 20 25 30  
65 Leu Gly Val Pro  
66 35  
69 <210> SEQ ID NO: 3  
70 <211> LENGTH: 54

Missing mandatory <220>, <223>  
features to explain the source  
of the artificial sequence. See  
#12 on the Error Summary Sheet.

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Input Set : A:\Sj-0005.app

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```

71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 3
75 Met Trp Leu Arg Ala Phe Ile Leu Ala Thr Leu Ser Ala Ser Ala Ala
76   1           5           10           15
78 Trp Gly His Pro Ser Ser Pro Pro Val Val Asp Thr Val His Gly Lys
79           20           25           30
81 Val Leu Gly Lys Phe Val Ser Leu Glu Gly Phe Ala Gln Pro Val Ala
82           35           40           45
84 Ile Phe Leu Gly Ile Pro
85   50
88 <210> SEQ ID NO: 4
89 <211> LENGTH: 54
90 <212> TYPE: PRT
91 <213> ORGANISM: Rattus sp.
93 <400> SEQUENCE: 4
94 Met Trp Leu Cys Ala Leu Val Trp Ala Ser Leu Ala Val Cys Pro Ile
95   1           5           10           15
97 Trp Gly His Pro Ser Ser Pro Pro Val Val Asp Thr Thr Lys Gly Lys
98           20           25           30
100 Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Phe Thr Gln Pro Val Ala
101           35           40           45
103 Val Phe Leu Gly Val Pro
104   50
107 <210> SEQ ID NO: 5
108 <211> LENGTH: 54
109 <212> TYPE: PRT
110 <213> ORGANISM: Mus musculus
112 <400> SEQUENCE: 5
113 Met Trp Leu His Ala Leu Val Trp Ala Ser Leu Ala Val Cys Pro Ile
114   1           5           10           15
116 Leu Gly His Ser Leu Leu Pro Pro Val Val Asp Thr Thr Gln Gly Lys
117           20           25           30
119 Val Leu Gly Lys Tyr Ile Ser Leu Glu Gly Phe Glu Gln Pro Val Ala
120           35           40           45
122 Val Phe Leu Gly Val Pro
123   50
126 <210> SEQ ID NO: 6
127 <211> LENGTH: 5
128 <212> TYPE: PRT
129 <213> ORGANISM: Oryctolagus cuniculus
131 <400> SEQUENCE: 6
132 His Pro Ser Ala Pro
133   1           5
136 <210> SEQ ID NO: 7
137 <211> LENGTH: 14
138 <212> TYPE: DNA
139 <213> ORGANISM: Oryctolagus cuniculus
141 <400> SEQUENCE: 7

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## RAW SEQUENCE LISTING

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Input Set : A:\Sj-0005.app

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142 cacccaagcg cacc 14
144 <210> SEQ ID NO: 8
145 <211> LENGTH: 14
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
152 <220> FEATURE:
153 <221> NAME/KEY: unsure
154 <222> LOCATION: (6)
156 <220> FEATURE:
157 <221> NAME/KEY: unsure
158 <222> LOCATION: (12)
160 <400> SEQUENCE: 8
W--> 161 caccnagcg cncc 14
163 <210> SEQ ID NO: 9
164 <211> LENGTH: 14
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
171 <220> FEATURE:
172 <221> NAME/KEY: unsure
173 <222> LOCATION: (6)
175 <220> FEATURE:
176 <221> NAME/KEY: unsure
177 <222> LOCATION: (9)
179 <220> FEATURE:
180 <221> NAME/KEY: unsure
181 <222> LOCATION: (12)
183 <400> SEQUENCE: 9
W--> 184 caccntcng cncc 14
186 <210> SEQ ID NO: 10
187 <211> LENGTH: 7
188 <212> TYPE: PRT
189 <213> ORGANISM: Oryctolagus cuniculus
191 <400> SEQUENCE: 10
192 Ala Phe Trp Thr Glu Leu Trp
193 1 5
196 <210> SEQ ID NO: 11
197 <211> LENGTH: 21
198 <212> TYPE: DNA
199 <213> ORGANISM: Oryctolagus cuniculus
201 <400> SEQUENCE: 11
202 gcattctgga cagaactatg g 21
204 <210> SEQ ID NO: 12
205 <211> LENGTH: 21
206 <212> TYPE: DNA
207 <213> ORGANISM: Oryctolagus cuniculus

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Input Set : A:\Sj-0005.app  
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```

209 <400> SEQUENCE: 12
210 ccaaagttca gtccagaaag c                               21
212 <210> SEQ ID NO: 13
213 <211> LENGTH: 21
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
220 <220> FEATURE:
221 <221> NAME/KEY: unsure /
222 <222> LOCATION: (4)
224 <220> FEATURE:
225 <221> NAME/KEY: unsure /
226 <222> LOCATION: (10)
228 <220> FEATURE:
229 <221> NAME/KEY: unsure /
230 <222> LOCATION: (19)
232 <400> SEQUENCE: 13
W--> 233 ccanagttcn gtccagaang c                               21
235 <210> SEQ ID NO: 14
236 <211> LENGTH: 21
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
243 <220> FEATURE:
244 <221> NAME/KEY: unsure /
245 <222> LOCATION: (10)
247 <220> FEATURE:
248 <221> NAME/KEY: unsure /
249 <222> LOCATION: (19)
251 <400> SEQUENCE: 14
W--> 252 ccataattcn gtccagaang c                               21
254 <210> SEQ ID NO: 15
255 <211> LENGTH: 30
256 <212> TYPE: PRT
257 <213> ORGANISM: Oryctolagus cuniculus
259 <400> SEQUENCE: 15
260 Met Trp Leu Cys Ala Leu Ala Leu Ala Ser Leu Ala Ala Cys Thr Ala
261   1           5           10           15
263 Trp Gly His Pro Ser Ala Pro Pro Val Val Asp Thr Val Lys
264   20           25           30
267 <210> SEQ ID NO: 16
268 <211> LENGTH: 30
269 <212> TYPE: PRT
270 <213> ORGANISM: Rattus sp.
272 <400> SEQUENCE: 16
273 Met Trp Leu Cys Ala Leu Val Trp Ala Ser Leu Ala Val Cys Pro Ile
274   1           5           10           15

```

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Input Set : A:\Sj-0005.app  
 Output Set: N:\CRF3\05072001\I595682A.raw

```

276 Trp Gly His Pro Ser Ser Pro Pro Val Val Asp Thr Thr Lys
277           20                      25                      30
280 <210> SEQ ID NO: 17
281 <211> LENGTH: 30
282 <212> TYPE: PRT
283 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 17
286 Met Trp Leu Arg Ala Phe Ile Leu Ala Thr Leu Ser Ala Ser Ala Ala
287   1                      5                      10                      15
289 Trp Gly His Pro Ser Ser Pro Pro Val Val Asp Thr Val His
290           20                      25                      30
293 <210> SEQ ID NO: 18
294 <211> LENGTH: 30
295 <212> TYPE: PRT
296 <213> ORGANISM: Rattus sp.
298 <400> SEQUENCE: 18
299 Met Arg Leu Tyr Pro Leu Val Trp Leu Phe Leu Ala Ala Cys Thr Ala
300   1                      5                      10                      15
302 Trp Gly Tyr Pro Ser Ser Pro Pro Val Val Asn Thr Val Lys
303           20                      25                      30
306 <210> SEQ ID NO: 19
307 <211> LENGTH: 30
308 <212> TYPE: PRT
309 <213> ORGANISM: Mus musculus
311 <400> SEQUENCE: 19
312 Met Trp Leu His Ala Leu Val Trp Ala Ser Leu Ala Val Cys Pro Ile
313   1                      5                      10                      15
315 Leu Gly His Ser Leu Leu Pro Pro Val Val Asp Thr Thr Gln
316           20                      25                      30
319 <210> SEQ ID NO: 20
320 <211> LENGTH: 1717
321 <212> TYPE: DNA
322 <213> ORGANISM: Oryctolagus cuniculus
324 <400> SEQUENCE: 20
325 gaattctgcc atgtggctct gtgcattggc cctggcctct ctgcgcgctt gcacggcttg 60
326 ggggcacccg tctgcaccac ctgtggtaga tactgtgcat ggcaaagtcc tggggaagtt 120
327 cgtcagctta gaaggatttg cacagcccggt ggccgtcttc ctgggagtc ccttcgccaa 180
328 gccccctctt ggatccctga ggtttgcacc accacagcct gcagaatcat tgagccacgt 240
329 gaagaacacc acctcctacc ctcccatgtg ctcccaggac gcagtatcag ggcatatgct 300
330 ctcgagagctc ttcaccaaca gaaaagagaa catccctctt aagttttctg aagactgcct 360
331 ttacctgaat atttacaccc ctgctgacct gacaaagaga ggcaggctgc cggatgatgt 420
332 gtggatccat ggaggtggtc tgatgggtgg tggagcatca acctatgatg gctggctct 480
333 ttctgcccac gagaacgtgg tgggtgtgac cattcagtag cgctgggca tctggggatt 540
334 cttcagcaca ggagatgagc acagccgagg gaactggggt cacttgacc aggtggctgc 600
335 gctgcggtgg gtccaggaca acattgccaa ctttgagggt gaccaggct ctgtgacct 660
336 ctttgagagag tcagcaggag gtcaaagtgt ctctatcctt ctattatccc ccctgaccaa 720
337 gaatctcttc catcgagcaa ttccgagag tggcgtggcc ctctttcca gtctcttcag 780
338 gaagaacacc aagtccttgg ctgagaaaat tgccatcgaa gctgggtgta aaaccaccac 840
339 ctcggtctgc atggttcaact gcctgcgcca gaagacagag gaagaactca tggaggtgac 900

```

## VERIFICATION SUMMARY

DATE: 05/07/2001

PATENT APPLICATION: US/09/595,682A

TIME: 17:38:04

Input Set : A:\Sj-0005.app

Output Set: N:\CRF3\05072001\I595682A.raw

L:42 M:258 W: Mandatory Feature missing, &lt;223&gt; OTHER INFORMATION:

L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/595682A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)                     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☒ Use of <220>Feature (NEW RULES)      Sequence(s)   1   are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.